

Title: US-10-005-647-1

RESULT 4

AF003927

LOCUS AF003927 3532 bp mRNA linear MAM 17-APR-2001
DEFINITION Bos taurus D-glucuronyl C5 epimerase mRNA, complete cds.
ACCESSION AF003927
VERSION AF003927.2 GI:13654638

KEYWORDS

SOURCE Bos taurus (cow)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.

REFERENCE 1 (bases 1 to 3532)
AUTHORS Li, J., Hagner-McWhirter, A., Kjellen, L., Palgi, J., Jalkanen, M. and Lindahl, U.

TITLE Biosynthesis of heparin/heparan sulfate. cDNA cloning and expression of D-glucuronyl C5-epimerase from bovine lung

J. Biol. Chem. 272 (44), 28158-28163 (1997)

MEDLINE 98010666

PUBMED 9346972

REFERENCE 2 (bases 1 to 3532)

AUTHORS Li, J.-P. and Lindahl, U.

TITLE Direct Submission

JOURNAL Submitted (14-MAY-1997) Medical and Physiological Chemistry, Biomedical Center, Husargatan 3, Uppsala 751 23, Sweden

REFERENCE 3 (bases 1 to 3532)

AUTHORS Li, J.-P., Gong, F., Darwish, K.E.I., Jalkanen, M. and Lindahl, U.

TITLE Direct Submission

JOURNAL Submitted (26-FEB-2001) Medical Chemistry and Microbiology, Biomedical Center, Husargatan 3, Uppsala 751 23, Sweden

REMARK Sequence update by submitter

COMMENT On Apr 17, 2001 this sequence version replaced gi:2465198.

FEATURES

Location/Qualifiers

source 1. .3532

/organism="Bos taurus"

/mol_type="mRNA"

/db_xref="taxon:9913"

/tissue_type="lung"

CDS 1. .1854

/function="heparin/heparan sulfate biosynthesis"

/codon_start=1

/product="D-glucuronyl C5 epimerase"

/protein_id="AAB72083.2"

/db_xref="GI:13654639"

/translation="MRCLAARVNYKTLIIICALFTLVTVLIWNKCSSDKAIQVPRHLS
SGFRVDALEKKAASESNNYVNHMAKQSEEAFFPQEQQKAPPVVGFFNNNGGGRVLGLK
YEEIDCLINDEHTIKGRREGNEVFLPFTWVEKYFDVYGKVVQYDGYDRFEFSHSYSKV
YAQRAPYHPDGVFMSFEGYNVEVRDRVKCISGVEGVPLSTQWGPQGYFYPIQIAQYGL
SHYSKNLTKPPHIEVYETAEDRDKNKPNPDWTVPKGCFMASVADKSRFTNVKQFIAP
ETSEGVSLQLGNTKDFIISFDLKFLTNGSVSVVLETTTEKNQLFTVHYVSNTQLIAFKE
RDIYYGIGPRTSWSTVTRDLVTDLRKGVGLSNTKAVKPTRIMPKKVVRLIAKKGFLD
NITISTTAHMAAFFAASDWLVNRQDEKGGWPIIMVTRKLGEFGKSLLEPGWYSAMAQQQA
ISTLVRAYLLTKDHIFLNSALRATAPYKFLSEQHGVKAVFMNKHWDWYEEYPTTPSSFV
LNGFMYSLIGLYDLKETAGEKLGKEARSLYERGMSLKAMLPDYDTGSGTIYDLRHF
LGIAPNLRWDYHTTHINQLQLLSTIDESPIFKEFVKRWKSYLKGSRAKHN"

ORIGIN

Query Match 85.1%; Score 1577.2; DB 4; Length 3532;
Best Local Similarity 91.0%; Pred. No. 0;
Matches 1688; Conservative 0; Mismatches 163; Indels 3; Gaps 1;

Qy 1 ATGCGTTGTTTGGCAGCTCGGGTCAACTATAAGACTTTGATTATCATCTGTGCGCTATTC 60
|||||

Db 1 ATGCGTTGTTTGGCAGCTCGGGTCAACTATAAGACTCTGATTATCATCTGCGCACTCTTC 60

Qy 61 ACTTTGGTCACAGTACTTTTGTGGAATAAGTGTTCCAGCGACAAAGCAATCCAGTTTCCT 120
 |||||
 Db 61 ACTTTGGTCACAGTACTTTTGTGGAATAAGTGTTCCAGTGACAAAGCGATCCAGGTTCCA 120

Qy 121 CGGCACTTGAGTAGTGGATTGAGAGTGGATGGATTAGAAAAAAGATCAGCAGCATCTGAA 180
 |||||
 Db 121 CGGCACTTGAGTAGTGGCTTCAGAGTGGATGCCTTAGAAAAAAGCAGCAGCGTCTGAG 180

Qy 181 AGTAACCACTATGCCAACACATAGCCAAACAGCAGTCAGAAGAGGCATTTCTCAGGAA 240
 || ||| ||||| ||||| ||| ||||| || ||||| || |||||
 Db 181 AGCAACAACCTATGTGAACCACATGGCCA---AGCAGTCTGAGGAGGCCTTCCCTCAGGAA 237

Qy 241 CAACAGAAGGCACCCCCTGTTGTTGGGGGCTTCAATAGCAACGGGGGAAGCAAGGTGTTA 300
 || ||||| || |||||
 Db 238 CAGCAGAAAAGCGCCCCTGTTGTTGGGGGCTTCAATAACAATGGGGGAGGCAGGGTGTTA 297

Qy 301 GGGCTCAAATATGAAGAGATTGACTGTCTCATAAACGATGAGCACACCATTAAGGGAGA 360
 |||||
 Db 298 GGGCTCAAATATGAAGAAATTGACTGCCTCATAAATGATGAACACACAATTAAAGGGAGA 357

Qy 361 CGAGAGGGGAATGAAGTTTTCTTCCATTCACTTGGGTAGAGAAATACTTTGATGTTTAT 420
 |||||
 Db 358 CGAGAGGGGAATGAAGTCTTTCTTCCATTACCTGGGTAGAGAAATATTTTGACGTTTAC 417

Qy 421 GGAAAAGTGGTCCAGTATGACGGCTATGATCGATTTGAATTCTCTCATAGCTATTCCAAA 480
 |||||
 Db 418 GGAAAGGTGGTTCAGTATGATGGCTATGATCGGTTTGAATTCTCTCATAGCTATTCCAAA 477

Qy 481 GTCTATGCACAGAGATCACCTTATCACCTGACGGTGTGTTTATGTCCTTTGAAGGCTAC 540
 |||||
 Db 478 GTCTATGCACAGAGAGCCCCTTATCACCTGATGGTGTGTTTATGTCCTTTGAAGGCTAC 537

Qy 541 AATGTGGAAGTCCGAGACAGAGTCAAATGTATAAGTGGAGTTGAAGGTGTGCCATTATCT 600
 |||||
 Db 538 AATGTGGAAGTCCGAGACAGAGTCAAGTGCATAAGTGGGGTTGAAGGTGTACCTTTATCT 597

Qy 601 ACCCAGTGGGGGCTCAAGGCTATTTCTACCCAATCCAGATTGCACAGTATGGGCTAAGT 660
 || |||||
 Db 598 ACACAGTGGGGACCTCAAGGCTATTTCTACCCAATCCAGATTGCACAGTATGGGTTAAGT 657

Qy 661 CATTACAGCAAGAATCTAACCGAGAAACCCCCTCACATAGAAGTATATGAAACAGCAGAA 720
 || |||||
 Db 658 CACTACAGCAAGAATCTAACTGAAAAACCCCCTCATATAGAGGTATATGAAACAGCAGAA 717

Qy 721 GACAGGGACAGAAACATCAGACCTAATGAATGGACTGTGCCAAGGGGTGCTTCATGGCC 780
 |||||
 Db 718 GACAGGGACAAAAACAGCAAGCCCAATGACTGGACTGTGCCAAGGGGTGCTTTATGGCT 777

Qy 781 AGTGTGGCAGACAAGTCTAGATCCACCAATGTTAAACAGTTTATTGCTCCAGAAACCAGT 840
 |||||
 Db 778 AGTGTGGCTGATAAGTCAAGATTACCAATGTTAAACAGTTCATTGCTCCAGAAACCAGT 837

Qy 841 GAAGGTGTGTCTTTGCAGCTGGGAAACACAAAAGACTTCATTATTTTCACTTGACCTCAAG 900
 |||||
 Db 838 GAAGGTGTATCCTTGCAACTGGGGAACACAAAAGATTATTATTTCATTTGACCTCAAG 897

Qy 901 CTTTTAACAAATGGGAGTGTGTCTGTGGTCTGGAGACCACAGAAAAGAATCAGCTCTTC 960
 | |||||
 Db 898 TTCTTAACAAATGGAAGCGTGTCTGTGGTCTGGAGACGACAGAAAAGAATCAGCTCTTC 957

Qy 961 ACTGTGCATTATGTCTCAAACACCCAGCTGATTGCTTTCAGAGACAGGGACATATACTAC 1020
 |||||
 Db 958 ACTGTACATTATGTCTCAAATACCCAGCTAATTGCTTTTAAAGAAAGAGACATATACTAT 1017

Qy 1021 GGCATTGGGCCCAGAACTTCATGGAGTACAGTTACCAGAGACCTGGTCACTGACCTCAGG 1080
 |||||
 Db 1018 GGCATCGGGCCCAGAACATCATGGAGCACAGTTACCCGGGACCTGGTCACTGACCTCAGG 1077

Qy	1081	AAAGGAGTGGGCCTTTCTAACACAAAAGCTGTCAAGCCAACCAAAATCATGCCCAAAAAAG	1140
Db	1078	AAAGGAGTGGGTCTTTCCAACACAAAAGCTGTCAAGCCAACAAGAATAATGCCCAAGAAG	1137
Qy	1141	GTGGTTAGGTTGATTGCAAAAGGGAAGGGATTCTCGGACAACATTACCATCTCAACCACA	1200
Db	1138	GTGGTTAGGTTGATTGCGAAAGGGAAGGGCTTCTTGACAACATTACCATCTCTACCACA	1197
Qy	1201	GCCCACATGGCTGCATTCTTTGCTGCAAGTGACTGGCTAGTGAGGAACCAGGATGAGAAA	1260
Db	1198	GCCCACATGGCTGCCTTCTTCGCTGCCAGTGACTGGCTGGTGAGGAACCAGGATGAGAAA	1257
Qy	1261	GGTGGCTGGCCAATTATGGTGACCCGGAAGTTAGGGGAAGGGTTTAAATCTTTAGAACCA	1320
Db	1258	GGCGGCTGGCCGATTATGGTGACCCGTAAGTTAGGGGAAGGCTTCAAGTCTTTAGAGCCA	1317
Qy	1321	GGATGGTACTCTGCCATGGCACAAGGGCAAGCCATCTCTACCTTAGTCAGGGCCTATCTT	1380
Db	1318	GGGTGGTACTCCGCCATGGCCAAGGGCAAGCCATTTCTACATTAGTCAGGGCCTATCTC	1377
Qy	1381	CTAACGAAAGACTATGTATTCTCAGTTCAGCTTTAAGGGCAACAGCCCCATACAAGTTT	1440
Db	1378	TTAACAAAAGACCATATATTCTCAATTCAGCTTTAAGGGCAACAGCCCCTTACAAGTTT	1437
Qy	1441	CCGTCAGAGCAGCATGGAGTTAAAGCCGTGTTTCATGAATAAACATGACTGGTATGAAGAA	1500
Db	1438	CTGTCAGAGCAGCATGGAGTCAAGGCTGTGTTTATGAATAAACATGACTGGTATGAAGAA	1497
Qy	1501	TATCCAACCACACCTAGCTCTTTTGTTTTAAATGGCTTTATGTATTCTTTAATTGGGCTG	1560
Db	1498	TATCCAACCTACACCTAGCTCTTTTGTTTTAAATGGCTTTATGTATTCTTTAATTGGGCTG	1557
Qy	1561	TATGACCTAAAAGAAACAGCAGGGGAGACACTTGGGAAAGAAGCAAGGTCCTTGTACGAG	1620
Db	1558	TATGACTTAAAAGAAACTGCAGGGGAAAAACTCGGGAAAGAAGCGAGGTCCTTGTATGAG	1617
Qy	1621	CGCGGCATGGAATCTCTTAAAGCCATGCTGCCCTTGATGATACTGGCTCCGGGACCATC	1680
Db	1618	CGTGGCATGGAATCCCTTAAAGCCATGCTCCCCTTGACGACACTGGCTCAGGAACCATC	1677
Qy	1681	TATGACCTCCGCCACTTCATGCTTGGCATTGCTCCCAACCTGGCCCCTGGGACTATCAC	1740
Db	1678	TATGACCTCCGGCACTTCATGCTTGGCATTGCCCCAACCTGGCCCCTGGGACTATCAC	1737
Qy	1741	ACCACCCACATTAACCAGCTGCAGCTGCTCAGCACCATCGATGAGTCCCCAATCTTCAA	1800
Db	1738	ACCACCCACATCAATCAACTGCAGCTGCTTAGCACCATTGATGAGTCCCCAATCTTCAA	1797
Qy	1801	GAATTTGTCAAGAGGTGGAAGAGCTACCTTAAAGGCAGTAGGGCAAAGCACAAC	1854
Db	1798	GAATTTGTCAAGAGGTGGAAGAGCTACCTTAAAGGCAGCCGGGCAAAGCACAAC	1851

Title: US-10-005-647-2

RESULT 6

AAW79263

ID AAW79263 standard; protein; 444 AA.

XX

AC AAW79263;

XX

DT 15-FEB-1999 (first entry)

XX

DE Bovine glucuronyl C5-epimerase.

XX

KW Glucuronyl C5-epimerase; cattle; D-glucuronic acid; L-iduronic acid;

KW heparin; heparan sulphate.

XX

OS Bos taurus.

XX

FH Key Location/Qualifiers

FT Region 25. .45

FT /note= "potential transmembrane region"

FT Modified-site 51

FT /note= "N-glycosylated"

FT Modified-site 130

FT /note= "N-glycosylated"

FT Modified-site 220

FT /note= "N-glycosylated"

XX

PN WO9848006-A1.

XX

PD 29-OCT-1998.

XX

PF 17-APR-1998; 98WO-SE000703.

XX

PR 18-APR-1997; 97SE-00001454.

XX

PA (LIND/) LINDAHL U.

PA (LIJJ/) LI J.

XX

PI Lindahl U, Li J;

XX

DR WPI; 1998-583655/49.

DR N-PSDB; AAV62688.

XX

PT DNA sequence coding for mammalian glucuronyl C5-epimerase and functional

PT derivatives - capable of converting D-glucuronic acid to L-iduronic acid

PT in the synthesis of heparin and heparan sulphate.

XX

PS Disclosure; Page 18-19; 26pp; English.

XX

CC This is the amino acid sequence of bovine glucuronyl C5-epimerase. It was

CC deduced from the sequence (see AAV62688) of a cDNA clone obtained from a

CC bovine lung cDNA library. Glucuronyl C5-epimerase catalyses the

CC conversion of D-glucuronic acid (GlcA) to L-iduronic acid (IdoA). The

CC invention relates to isolated or recombinant DNA sequences for a

CC mammalian (including human) glucuronyl C5-epimerase or its functional

CC derivative. Recombinant expression vectors and transformed host cells are

CC also claimed. The nucleic acid and vector can be used for the recombinant

CC production of the enzyme. Glucuronyl C5-epimerase is useful for

CC converting GlcA to IdoA in the biosynthesis of heparin and heparan

CC sulphate

XX

SQ Sequence 444 AA;

Query Match 69.6%; Score 2271; DB 2; Length 444;

Best Local Similarity 96.8%; Pred. No. 1.3e-203;

Matches 430; Conservative 9; Mismatches 5; Indels 0; Gaps 0;

Qy	175	MSFEGYNVEVRDRVKCISGVEGVPLSTQWGPQGYFYPIQIAQYGLSHYSKNLTEKPPHIE	234
Db	1	MSFEGYNVEVRDRVKCISGVEGVPLSTQWGPQGYFYPIQIAQYGLSHYSKNLTEKPPHIE	60
Qy	235	VYETAEDRDRNIRPNEWTVPKGCFMASVADKSRSTNVKQFIAPETSEGVSLQLGNTKDFI	294
Db	61	VYETAEDRDKNSKPNDWTVPKGCFMASVADKSRFTNVKQFIAPETSEGVSLQLGNTKDFI	120
Qy	295	ISFDLKLTLNGSVSVVLETTTEKNQLFTVHYVSNTQLIAFRDRDIYYGIGPRTSWSTVTRD	354
Db	121	ISFDLKFLTNGSVSVVLETTTEKNQLFTVHYVSNTQLIAFKERDIYYGIGPRTSWSTVTRD	180
Qy	355	LVTDLRKGVGLSNTKAVKPTKIMPKKVRLIAKGKGFLDNITISTTAHMAAFFAASDWLV	414
Db	181	LVTDLRKGVGLSNTKAVKPTRIMPKKVRLIAKGKGFLDNITISTTAHMAAFFAASDWLV	240
Qy	415	RNQDEKGGWPIMVTRKLGEGFKSLEPGWYSAMAQQQAISTLVRAYLLTKDYVFLSSALRA	474
Db	241	RNQDEKGGWPIMVTRKLGEGFKSLEPGWYSAMAQQQAISTLVRAYLLTKDHIFLNSALRA	300
Qy	475	TAPYKFPSEQHGVKAVFMNKHWDWYEEYPTTPSSFVLNGFMYSLIGLYDLKETAGETLGKE	534
Db	301	TAPYKFLSEQHGVKAVFMNKHWDWYEEYPTTPSSFVLNGFMYSLIGLYDLKETAGEKLGKE	360
Qy	535	ARSLYERGMESLKAMLPDYDTGSGTIYDLRHFMLGIAPNLRWDYHTTHINQLQLLSTID	594
Db	361	ARSLYERGMESLKAMLPDYDTGSGTIYDLRHFMLGIAPNLRWDYHTTHINQLQLLSTID	420
Qy	595	ESPIFKEFVKRWKSYLKGSRAKHN	618
Db	421	ESPIFKEFVKRWKSYLKGSRAKHN	444

RESULT 15

US-09-403-269-13

; Sequence 13, Application US/09403269

; GENERAL INFORMATION:

; APPLICANT: ULF, Lindahl

; APPLICANT: LI, Jin-Ping

; TITLE OF INVENTION: DNA Sequence Coding for a Mammalian Glucuronyl C5-Epimerase and a

; TITLE OF INVENTION: Process for Its Production

; FILE REFERENCE: 003300-589

; CURRENT APPLICATION NUMBER: US/09/403,269

; CURRENT FILING DATE: 1999-10-18

; PRIOR APPLICATION NUMBER: SE 9701454-2

; PRIOR FILING DATE: 1997-04-18

; PRIOR APPLICATION NUMBER: PCT/SE98/00703

; PRIOR FILING DATE: 1998-04-17

; NUMBER OF SEQ ID NOS: 13

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 13

; LENGTH: 444

; TYPE: PRT

; ORGANISM: Human

US-09-403-269-13

Query Match 69.6%; Score 2271; DB 18; Length 444;
 Best Local Similarity 96.8%; Pred. No. 3e-220;
 Matches 430; Conservative 9; Mismatches 5; Indels 0; Gaps 0;

Qy	175	MSFEGYNVEVRDRVKCISGVEGVPLSTQWGPQGYFYPIQIAQYGLSHYSKNLTEKPPHIE	234
Db	1	MSFEGYNVEVRDRVKCISGVEGVPLSTQWGPQGYFYPIQIAQYGLSHYSKNLTEKPPHIE	60
Qy	235	VYETAEDRDRNIRPNEWTVPKGCFMASVADKSRSTNVKQFIAPETSEGVSLQLGNTKDFI	294
Db	61	VYETAEDRDKNSKPNDWTVPKGCFMASVADKSRFTNVKQFIAPETSEGVSLQLGNTKDFI	120

Qy 295 ISFDLKLTLNGSVSVVLETTEKNQLFTVHYVSNTQLIAFRDRDIYYGIGPRTSWSTVTRD 354
 ||||| :|||
 Db 121 ISFDLKLTLNGSVSVVLETTEKNQLFTVHYVSNTQLIAFKERDIYYGIGPRTSWSTVTRD 180
 Qy 355 LVTDLRKGVGLSNTKAVKPTKIMPKKVRLIAKGKGFLDNITISTTAHMAAFFAASDWLV 414
 ||||| :|||
 Db 181 LVTDLRKGVGLSNTKAVKPTRIMPKKVRLIAKGKGFLDNITISTTAHMAAFFAASDWLV 240
 Qy 415 RNQDEKGGWPIMVTRKLGEGFKSLEPGWYSAMAQQAISTLVRAYLLTKDYVFLSSALRA 474
 ||||| :|||
 Db 241 RNQDEKGGWPIMVTRKLGEGFKSLEPGWYSAMAQQAISTLVRAYLLTKDHFILNSALRA 300
 Qy 475 TAPYKFPSEQHGVKAVFMNKHWDWYEEYPTTPSSFVLNGFMYSLIGLYDLKETAGETLGKE 534
 ||||| |||
 Db 301 TAPYKFLSEQHGVKAVFMNKHWDWYEEYPTTPSSFVLNGFMYSLIGLYDLKETAGEKLGKE 360
 Qy 535 ARSLYERGMESLKAMLPDYDTGSGTIYDLRHFMLGIAPNLRWDYHTTHINQLQLLSTID 594
 ||||| |||
 Db 361 ARSLYERGMESLKAMLPDYDTGSGTIYDLRHFMLGIAPNLRWDYHTTHINQLQLLSTID 420
 Qy 595 ESPIFKEFVKRWKSYLKGSRAKHN 618
 |||||
 Db 421 ESPIFKEFVKRWKSYLKGSRAKHN 444

RESULT 1

GLCE_MOUSE

ID GLCE_MOUSE STANDARD; PRT; 618 AA.
 AC Q9EPS3; Q99MM0;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE D-glucuronyl C5-epimerase (EC 5.1.3.-) (Heparin/heparan
 DE sulfate:glucuronic acid C5 epimerase).
 GN GLCE.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A., TISSUE SPECIFICITY, AND FUNCTION.
 RC STRAIN=BALB/c; TISSUE=Liver, and Mast cells;
 RX MEDLINE=21282921; PubMed=11274177;
 RA Li J.-P., Gong F., El Darwish K., Jalkanen M., Lindahl U.;
 RT "Characterization of the D-glucuronyl C5-epimerase involved in the
 RT biosynthesis of heparin and heparan sulfate."
 RL J. Biol. Chem. 276:20069-20077(2001).
 RN [2]
 RP SEQUENCE FROM N.A., AND SUBCELLULAR LOCATION.
 RC TISSUE=Mast cells;
 RX MEDLINE=21293046; PubMed=11279150;
 RA Crawford B.E., Olson S.K., Esko J.D., Pinhal M.A.S.;
 RT "Cloning, Golgi localization, and enzyme activity of the full-length
 RT heparin/heparan sulfate-glucuronic acid C5-epimerase."
 RL J. Biol. Chem. 276:21538-21543(2001).
 CC -!- FUNCTION: Converts D-glucuronic acid residues adjacent to N-
 CC sulfate sugar residues to L-iduronic acids.
 CC -!- PATHWAY: Heparin and heparan sulfate biosynthesis.
 CC -!- SUBCELLULAR LOCATION: Type II membrane protein. Golgi.
 CC -!- TISSUE SPECIFICITY: Widely expressed with highest levels in lung
 CC and lowest levels in spleen.
 CC -!- SIMILARITY: Belongs to the D-glucuronyl C5-epimerase family.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its

